REMARKS

Applicant would like to thank the Examiner for the communication pointing out the inconsistent numbering as provided in the clean and marked up version of Claim 1 in the Office Action response filed on December 17, 2002. The Applicant submits a corrected version of the set of claims that corresponds with those claims as filed on December 17, 2003. The arguments as provided in the response of December 17, 2002 remain the same with regards to the currently provided claims. No substantive changes have been made to the claims and the correction was with regards to the numbering of the steps of Claim 1.

Based upon the corrected version of claims, as provided in the present communication, and the arguments previously provided in the response of December 17, 2002, the Applicant respectfully requests reconsideration of the present invention and allowance of the pending claims. If the Examiner should have any questions, please contact the undersigned for any further clarification. Applicant hereby requests further consideration of the application.

Respectfully submitted,

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By: _____

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CERTIFICATE OF EXPRESS MAILING

I hereby certify that the enclosed Amendment in Response to Office Action is being deposited with the United States Postal Service as Express Mail No. EU843550885US, postage prepaid, in an envelope addressed to the Assistant Commissioner for Patents, Washington, DC 20231, on this 17th day of April, 2003.

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Appendix A

(A Copy of the Marked Up Version)

1. (Twice Amended) A method of selection and/or identifying one or more protein affinity ligands, wherein the affinity ligands are antibodies, that bind to one or more proteins of interest, comprising the steps of:

(A) obtaining a real or theoretical mass spectrometry based characterization of the one or more proteins by either:

i. Subjecting the one or more proteins to a mass spectrometry based characterization; or

ii. Predicting the mass spectrometry based characterization from known data;

(B) utilizing the one or more proteins either individually or as a mixture to:

i. Generate one or more antibodies thereto by immunization; and/or

ii. Select, using a single or multiple rounds of binding, one or more antibodies thereto;

(C) screening to one or more antibodies generated in step B(i) and/or [the one or more] multiple antibodies selected by step (B)(ii) by:

i. adding a mixture of proteins or the one or more proteins individually [or as a mixture of proteins] to the one or more antibodies generated in step (B)(i) or the one or more antibodies selected in step (B)(ii), each antibody being used individually, and

ii. after removing any proteins which have not bound, eluting the at least one protein has bound;

(D) subjecting the at least one eluted protein to mass spectrometry based characterization; and

(E) by comparing the mass spectrometry based characterization obtains in steps (A) and (D), selecting and/or identifying that at least one antibody that binds to the one or more proteins of interest.

2. (Once Amended) A method as claimed in claim 1 wherein the one or more proteins of interest [are] have been previously resolved by 2D electrophoresis.

4. (Twice Amended) A method as claimed in claim 1 wherein the one [of] or more proteins of interest are present in a mixture of proteins.

5. (Twice Amended) A method as claimed in claim 1 wherein the method is a [shotgun] method for selecting and identifying protein affinity ligands to a plurality of proteins.

7. (Twice Amended) A method as claimed in claim 1 wherein the antibodies optionally generated in step (B)(i) are immobilized on a support comprising nitrocellulose or PVDF.

8. (Once Amended) A method as claimed in claim 7 wherein the support upon which the antibodies are immobilised and the nitrocellulose or PVDF are treated with an oligosaccharide or polyvinylpyrrolidine solution to block any remaining binding sites.

12. (Once Amended) A method generating monoclonal antibodies to one or more targeted proteins comprising the steps of:

(a) resolving a complex protein mixture;

(b) subjecting the resolved protein(s) to peptide mass fingerprinting to obtain a peptide mass profile or obtain a theoretical peptide mass profile;

(c) utilizing one or more of the resolved proteins to generate one or more monoclonal antibodies thereto;

(d) adding the or another complex protein mixture to the one or more monoclonal antibodies generated in Step (c), to select those proteins which bind the one or more monoclonal antibodies, and subjecting the selected proteins(s) to peptide mass fingerprinting to obtain a peptide mass profile;

(e) comparing the peptide mass profiles obtained in steps (b) and (d); and

(f) selecting one or more monoclonal antibodies [hybridoma clones] of interest.

13. (Once Amended) A method of generating an antibody library comprising the steps of:

(a) resolving a complex protein mixture and subjecting the resolved protein(s) to peptide mass finger printing to obtain a peptide mass profile; or

(b) obtaining a theoretical peptide mass profile for a protein which is sought;

(c) utilizing the or the other complex protein mixture to generate one or more monoclonal antibodies thereto;

(d) adding the one or the other complex protein mixture to the one or more monoclonal antibodies generated in Step (c) to select those proteins which bind

the one or more monoclonal antibodies, and subjecting the selected protein(s) to peptide mass fingerprinting to obtain a peptide mass profile;

(e) comparing the peptide mass profiles obtained in steps (a or b) and (d); and

(f) identifying the monoclonal antibodies of [potential] interest [for a monoclonal antibody library].

17. (Twice Amended) A method as claimed in claims 1, 2, 7, 8, or 9[, 10, 19, 20, 21, 22, 23, 24, 25, 26, or 27] wherein the mass spectrometry based characterization [peptide mass fingerprint] is obtained by mass spectrometry.

18. (Twice Amended) A method as claimed in claims 1, 2, 7, 8, or 9 [, 10, 19, 20, 21, 22, 23, 24, 25, 26, or 27] further comprising the use of automated well plate handling technology and automated high-throughput mass spectrometry.

29. (Once Amended) A method as claimed in claim 2 wherein the method is [shotgun] method for selecting and identifying protein affinity ligands to a plurality of proteins.

34. (Once Amended) A method of selecting and/or identifying at least one antibody which binds at least one protein of interest, comprising the steps of:

(a) obtaining a theoretical [pre-selected] mass spectrometry-based characterization of a target protein [to serve as a reference standard];

(b) providing an antibody which selectively binds to said target protein;

(c) isolating and collecting said target protein through affinity binding with said antibody;

(d) analyzing said collected target protein for said pre-selected mass spectrometry-based characterization; and

(e) comparing the mass spectrometry-based characterization obtained in step (d) with the theoretical mass spectrometry-based characterization [reference standard] of step (a).

37. (New) A method as claimed in claim 1 wherein an eluting agent is further provided for eluting protein from antibody-protein complexes.

38. (New) A method as claimed in claim 37 wherein the eluting agent is formic acid.

39. (New) A method as claimed in claim 8 wherein an eluting agent is further provided for eluting protein from antibody-protein complexes.

40. (New) A method as claimed in claim 39 wherein the eluting agent is formic acid.

41. (New) A method as claimed in claim 19 wherein an eluting agent is further provided for eluting protein from antibody-protein complexes.

42. (New) A method as claimed in claim 41 wherein the eluting agent is formic acid.

43. (New) A method as claimed in claim 20 wherein an eluting agent is further provided for eluting protein from antibody-protein complexes.

44. (New) A method as claimed in claim 43 wherein the eluting agent is formic acid.

45. (New) A method as claimed in claim 21 wherein an eluting agent is further provided for eluting protein from antibody-protein complexes.

46. (New) A method as claimed in claim 45 wherein the eluting agent is formic acid.